

putative polypeptide	number of amino acids	proposed function or sequence similarity detected	probability	start/stop codons	best match
CalA	328	membrane transporter (ATP-binding)	$5.4 \times 10^{-124}$	ATG/TGA	DtrA <sup>97</sup>
CalB	561	membrane transporter	$5.5 \times 10^{-70}$	ATG/TGA	DtrB <sup>97</sup>
CalC	181	calicheamicin resistance protein	confirmed	ATG/TGA	
CalD	263	O-methyltransferase	$1.1 \times 10^{-99}$	ATG/TGA	AveBVII <sup>98</sup>
CalE	420	glycosyltransferase	$4.7 \times 10^{-30}$	GTG/TAG	EryCII <sup>99</sup>
CalF	245	N,N-dimethyltransferase	$1.5 \times 10^{-78}$	ATG/TGA	DesVI <sup>100</sup>
CalG	990	TDP-D-glucose 4,6-dehydratase	confirmed	GTG/TAG	
CalH	338	Perosamine synthetase	confirmed	GTG/TGA	
CalI	568	Dipeptide transporter	$1.7 \times 10^{-24}$	GTG/TGA	DciAE
CalJ	332	O-methyltransferase	$1.0 \times 10^{-37}$	ATG/TGA	DmpM
CalK	440	L-cysteine/cystine C-S-lyase	$1.6 \times 10^{-28}$	GTG/TGA	C-DES
CalL	562	Oligopeptide transporter protein	$9.5 \times 10^{-14}$	ATG/TGA	OppA
CalM	416	Regulatory protein		GTG/TGA	
CalN	398	Glycosyltransferase	$3.4 \times 10^{-79}$	ATG/TGA	OleI
CalO	331	Hexopyranosyl-2,3-reductase	$4.9 \times 10^{-139}$	ATG/TGA	EryBII
CalP	(179)	Desaturase	$5.7 \times 10^{-7}$	/TGA	CrtI
CalQ	453	UDP-D-glucose 6-dehydrogenase	confirmed	GTG/TGA	
CalR	282	Transcriptional regulator	$6.7 \times 10^{-11}$	ATG/TGA	SC5C7.03
CalS	1113	P <sub>450</sub> oxidase	$2.9 \times 10^{-66}$	GTG/TGA	BioI
CalT	432	oxygenase/halogenase	$2.0 \times 10^{-62}$	GTG/TAA	PCZA361.20
CalU	377	glycosyltransferase	$2.0 \times 10^{-53}$	ATG/TGA	SnogE/D
CalV	125	$\beta$ -keto-acyl synthase III	$2.0 \times 10^{-65}$	ATG/TGA	SC4A9
CalW	(449)	cytochrome P450	$1.0 \times 10^{-91}$	GTG/TGA	CYP105B1
CalX	(197)	TDP-4-keto-6-deoxy-L-hexose 2,3-dehydratase	$1.0 \times 10^{-22}$	/TGA	MtmV
6MSAS	(198)	orsellenic acid synthase	$6.5 \times 10^{-76}$	ATG/	AviM
ActI	(207)	polyketide cyclase	$3.0 \times 10^{-66}$	/TGA	CurF
ActII	136	polyketide cyclase	$5.0 \times 10^{-53}$	ATG/TGA	SchB
ActIII	(308)	polyketide synthase	$8.6 \times 10^{-148}$	GTG/	PmsI
orf1	322	unknown		ATG/TGA	
orf2	654	unknown		ATG/TGA	
orf3	373	integrase	$3.0 \times 10^{-13}$	ATG/TGA	Yld
orf4	521	chromosome partitioning protein	$3.3 \times 10^{-10}$	GTG/TAA	ParA
orf5	175	unknown		ATG/TGA	
orf6	139	unknown		ATG/TGA	
orf7	187	unknown		GTG/TGA	
orf8	266	regulatory protein	$3.0 \times 10^{-66}$	ATG/TGA	KorSA
OrfI	127	hydroxylase	$1.5 \times 10^{-7}$	ATG/TGA	SC4C6.24c
OrfII	248	unknown		GTG/TGA	
OrfIII	298	hydroxylase	$3.3 \times 10^{-90}$	GTG/TGA	SCA32
OrfIV	363	unknown	$5.3 \times 10^{-43}$	GTG/TGA	SC9C7.25
OrfV	288	aminotransferase	$2.9 \times 10^{-37}$	GTG/TGA	SCF55
OrfVI	1012	glu-ammonia-ligase adenyltransferase	exact	GTG/TGA	SCA32
OrfVII	236	Methyltransferase	$8.0 \times 10^{-63}$	GTG/TAG	SCF43A.25c
OrfVIII	441	Integral membrane protein	$8.9 \times 10^{-9}$	GTG/TGA	SCA32
OrfIX	478	Integral membrane protein	$1.1 \times 10^{-21}$	ATG/TGA	MLB268
OrfX	504	Membrane protein	$5.5 \times 10^{-20}$	GTG/TGA	B1496.F1.14
OrfXI	251	Immunity resistance protein	$1.1 \times 10^{-9}$	ATG/TGA	TFXG
IS-element	1209 bp	insertional element	$5.7 \times 10^{-168}$		IS1136 <sup>111</sup>

FIG. 3

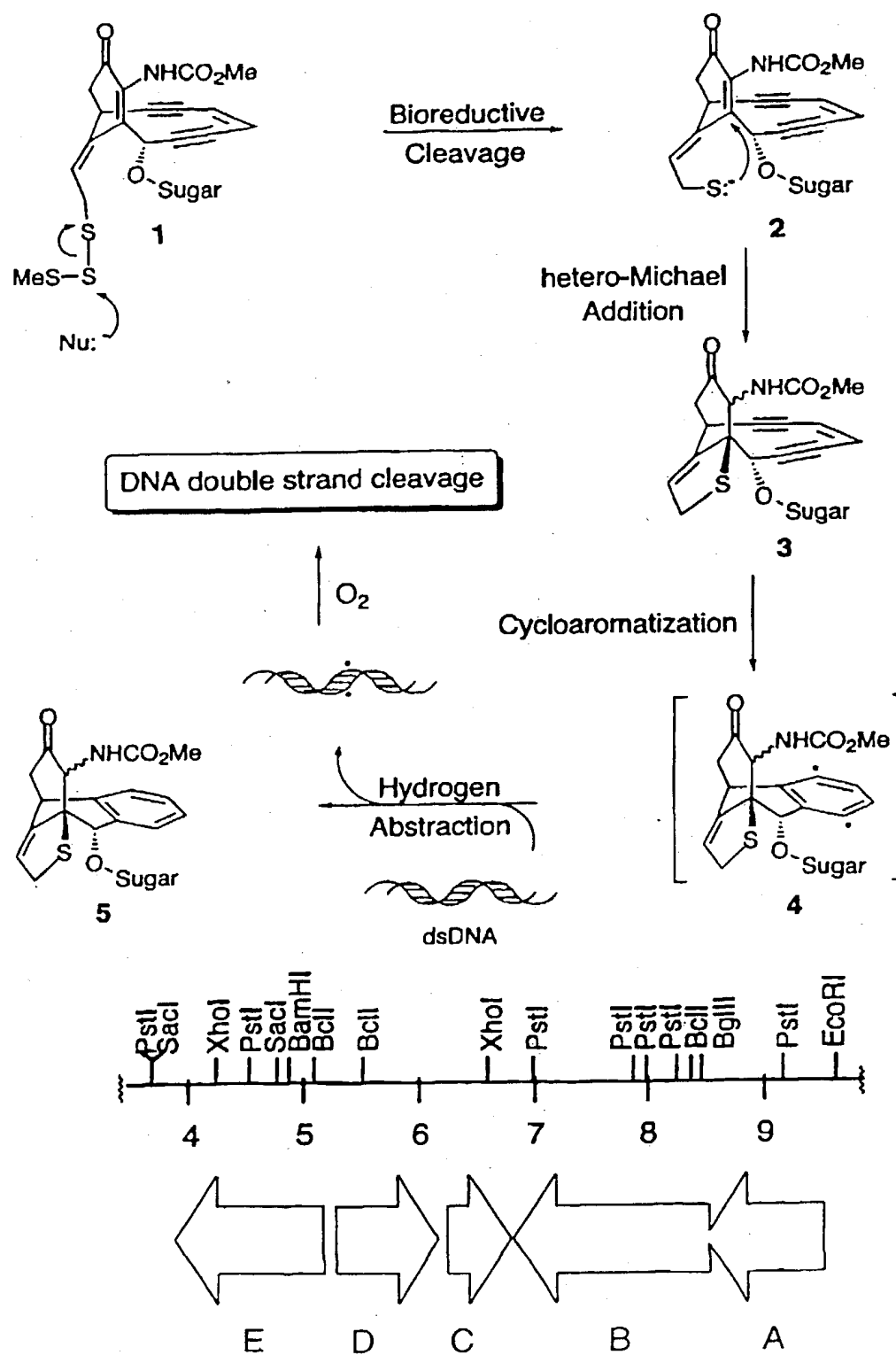


FIG. 12

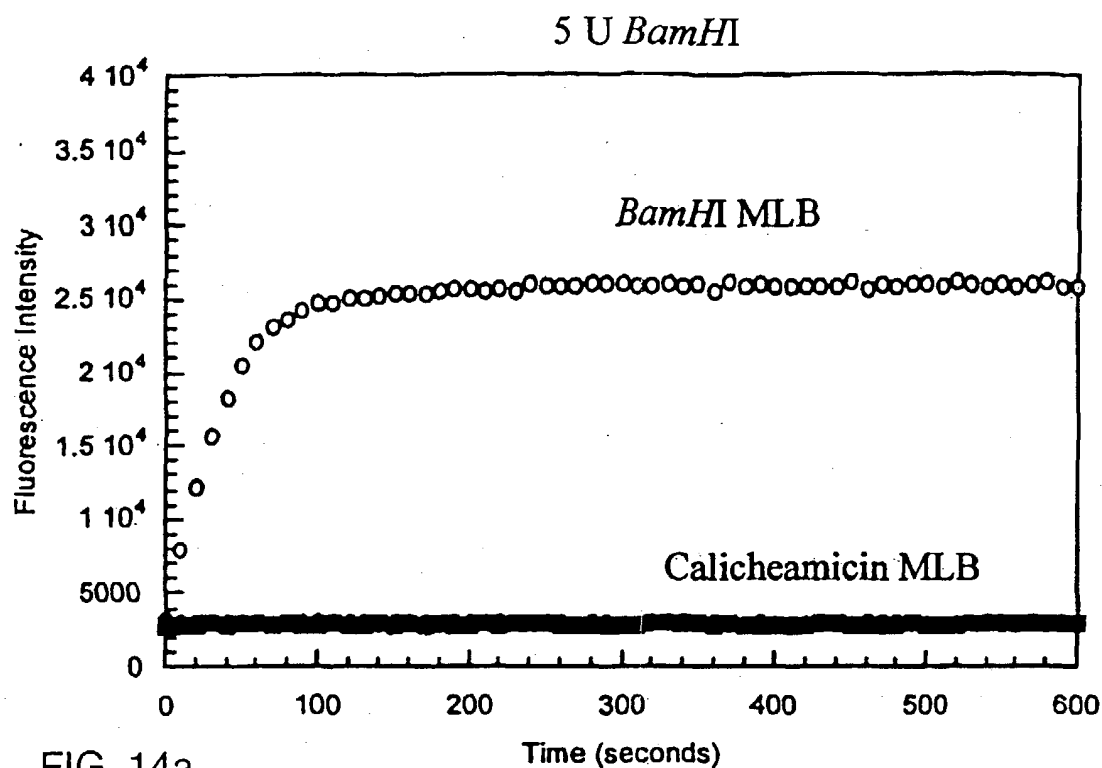


FIG. 14a

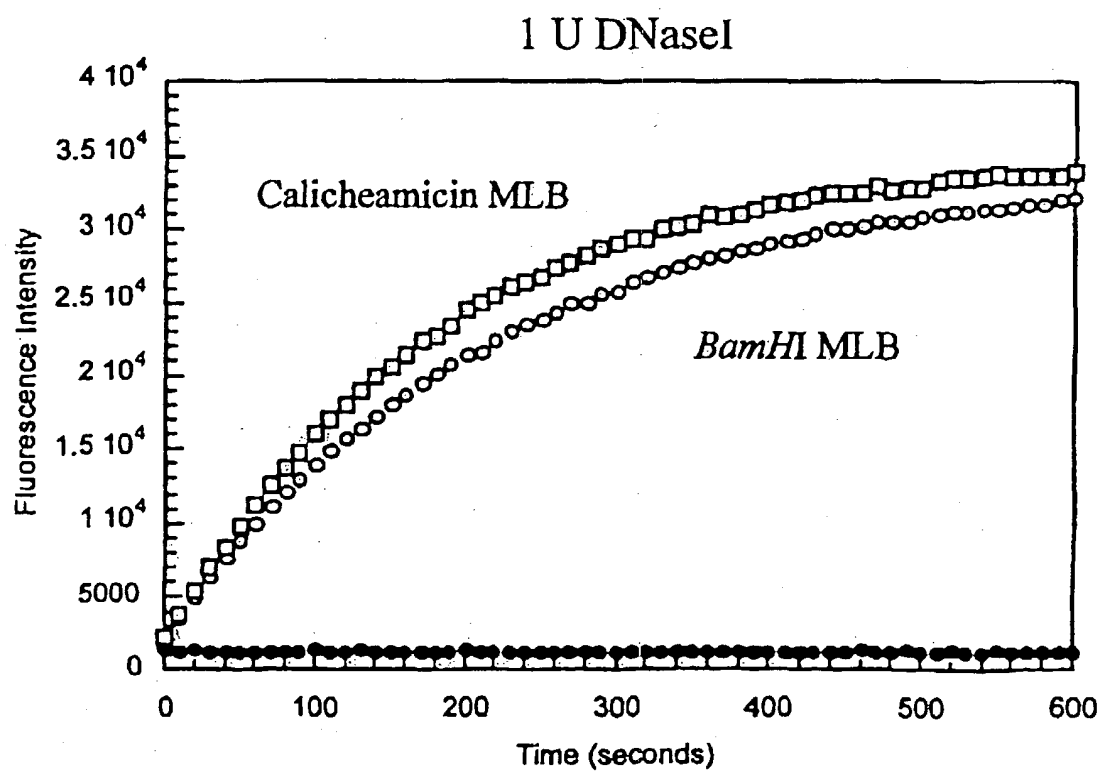


FIG. 14b

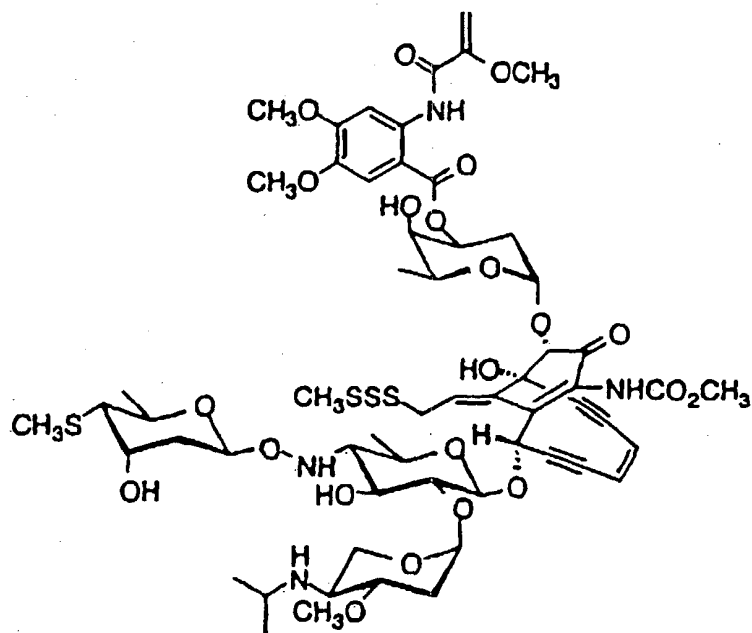
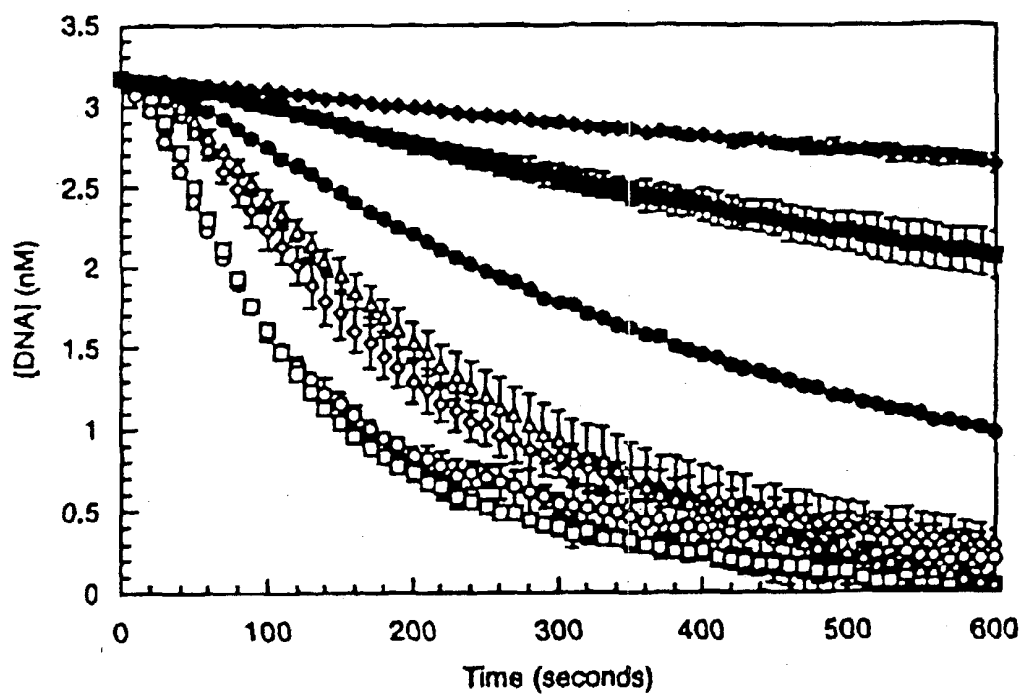


FIG. 15b